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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE 09/26/2001
TIME 23:02:37

INPUT SET: S36631

This Raw Listing contains the General
Information Section and up to the first 5 pages.

TELECENTER 1600/2900

NOV 13 2001

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SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ceriani, Roberto L.
6 Peterson, Jerry A.
7 Larocca, David J.
8
9 (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON
10 KIT & METHODS
11
12 (iii) NUMBER OF SEQUENCES: 5
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Ratner & Prestia
16 (B) STREET: Suite 301
17 One Westlakes, Berwyn
18 (C) CITY: Valley Forge
19 (D) STATE: Pennsylvania
20 (E) COUNTRY: USA
21 (F) ZIP: 19482
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk 3.5"
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
27 (D) SOFTWARE: PatentIn #1.0,
28 Version #1.25
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER: 08/482,596
32 (B) FILING DATE: June 7, 1995
33 (C) CLASSIFICATION:
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Amzel, Viviana
37 (B) REGISTRATION No.: 30,930
38 (C) REFERENCE/DOCKET No.: CRFC-046
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (610) 407-0700
42 (B) TELEFAX: (610) 407-0701
43 (C) TELEX: N.A.
44
45
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:37

INPUT SET: S36631.raw

47 (2) INFORMATION FOR SEQ ID NO:1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1384 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: both

53 (D) TOPOLOGY: linear
5455 (ii) MOLECULE TYPE: DNA
5657 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58

59	GATTTTCATCC	ATGATGTTAA	TAAAAAACAC	AAGGAGTTTG	TGGGTAAC TG	50
60	GAACAAAAAC	GCGGTGCATG	TCAACCTGTT	TGAGACCCCT	GTGGAGGCTC	100
61	AGTACGTGAG	ATTGTACCCC	ACGAGCTGCC	ACACGGCCTG	CACTCTGCGC	150
62	TTTGAGCTAC	TGGGCTGTGA	GCTGAACGGA	TGCGCCAATC	CCCTGGGCTT	200
63	GAAGAATAAC	AGCATCCCTG	ACAAGCAGAT	CACGGCCTCC	AGCAGCTACA	250
64	AGACCTGGGG	CTTGCATCTC	TTCAGCTGGA	ACCCCTCCTA	TGCACGGCTG	300
65	GACAAGCAGG	GCAACTTCAA	CGCCTGGGTT	GCGGGGAGCT	ACGGTAACGA	350
66	TCAGTGGCTG	CAGGTGGACC	TGGGCTCCTC	GAAGGAGGTG	ACAGGCATCA	400
67	TCACCCAGGG	GGCCCGTAAC	TTTGGCTCTG	TCCAGTTTGT	GGCATCCTAC	450
68	AAGGTTGCCT	ACAGTAATGA	CAGTGCGAAC	TGGACTGAGT	ACCAGGACCC	500
69	CAGGACTGGC	AGCAGTAAGA	TCTTCCCTGG	CAACTGGGAC	AACCACTCCC	550
70	ACAAGAAGAA	CTTGTTTGAG	ACGCCCATCC	TGGCTCGCTA	TGTGCGCATC	600
71	CTGCCTGTAG	CCTGGCACAA	CCGCATCGCC	CTGCGCCTGG	AGCTGCTGGG	650
72	CTGTTAGTGG	CCACCTGCCA	CCCCCAGGTC	TTCTTGCTTT	CCATGGGCCC	700
73	GCTGCCTCTT	GGCTTCTCAG	CCCCTTTAAA	TCACCATAGG	GCTGGGGACT	750
74	GGGGAAGGGG	AGGGTGTTCA	GAGGCAGCAC	CACCACACAG	TCACCCCTCC	800
75	CTCCCTCTTT	CCCACCTCC	ACCTCTCACG	GGCCCTGCCC	CAGCCCCTAA	850
76	GCCCCGTCCC	CTAACCCCCA	GTCCTCACTG	TCCTGTTTTT	TTAGGCACTG	900
77	AGGGATCTGA	GTAGTCTG	GATGGACAGG	AAAGGGCAAA	GTAGGGCGTG	950
78	TGTTTTCCCT	GCCCTGTCTT	GGACCGCCGA	TCCCAGGTGC	GTGTGTCTCT	1000
79	GTCTCTCCTA	GCCCTCTCTT	CACACATCAC	ATTCCCATGG	TGGCCTCAAG	1050
80	AAAGGCCCGG	AAGCCCCAGG	CTGGAGATAA	CAGCCTCTTG	CCCGTCGGCC	1100
81	CTGCGTCGGC	CCTGGGGTAC	CATGTGCCAC	AACTGCTGTG	GCCCCCTGTC	1150
82	CCCAAGACAC	TTCCCCTTGT	CTCCCTGGTT	GCCTCTCTTG	CCCCTTGTCC	1200
83	TGAAGCCCAG	CGACACAGAA	GGGGGTGGGG	CGGGTCTATG	GGGAGAAAGG	1250
84	GAGCGAGGTC	AGAGGAGGGC	ATGGGTGGGC	AGGGTGGGCG	TTTGGGGCCC	1300
85	TCATGCTGGC	TTTTCACCCC	AGAGGACACA	GGCAGCTTCC	AAAATATATT	1350
86	TATCTTCTTC	ACGGGAAAAA	AAAAAAAAAA	ACCG		

1384

87
88
89
90 (2) INFORMATION FOR SEQ ID NO:2:91
92 (i) SEQUENCE CHARACTERISTICS:

93 (A) LENGTH: 218 amino acids

94 (B) TYPE: amino acid

95 (C) STRANDEDNESS:

96 (D) TOPOLOGY: linear
9798 (ii) MOLECULE TYPE: protein
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:37

INPUT SET: S36631.raw

100 (v) FRAGMENT TYPE:

101

102

103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

104

105 Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val

106 1 5 10

107 Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu

108 15 20 25

109 Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser

110 30 35 40

111 Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys

112 45 50 55

113 Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn

114 60 65 70

115 Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys

116 75 80

117 Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala

118 85 90 95

119 Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly

120 100 105 110

121 Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser

122 115 120 125

123 Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn

124 130 135 140

125 Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr

126 145 150

127 Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg

128 155 160 165

129 Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His

130 170 175 180

131 Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg

132 185 190 195

133 Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala

134 200 205 210

135 Leu Arg Leu Glu Leu Leu Gly Cys

136 215

137

138

139

140 (2) INFORMATION FOR SEQ ID NO:3:

141

142 (i) SEQUENCE CHARACTERISTICS:

143 (A) LENGTH: 217

144 (B) TYPE: amino acid

145 (C) STRANDEDNESS:

146 (D) TOPOLOGY: linear

147

148 (ii) MOLECULE TYPE: protein

149

150 (v) FRAGMENT TYPE:

151

152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:38

INPUT SET: S36631.raw

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153
154 Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
155 1 5 10
156 Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
157 15 20 25
158 Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
159 30 35 40
160 His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
161 45 50 55
162 Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
163 60 65 70
164
165 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr
166 75 80
167 Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
168 85 90 95
169 Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser
170 100 105 110
171 Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser Ser
172 115 120 120
173 Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn Phe
174 130 135 140
175 Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr Ser
176 145 150
177 Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr
178 155 160 165
179 Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
180 170 175 180
181 His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr
182 185 190 195
183 Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu
184 200 205 210
185 Arg Leu Glu Leu Leu Gly Cys
186 215 217
187
188
189

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

202 Phe Lys Gly Asn Ser Thr Arg Asn Val Met Tyr Phe Asn Gly
203 1 5 10
204
205

```

RAW SEQUENCE LISTING PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:38

INPUT SET: S36631.raw

```

206 Asn Ser Asp Ala Ser Thr Ile Lys Glu Asn Gln Phe Asp Pro
207 15 20 25
208 Pro Ile Val Ala Arg Tyr Ile Arg Ile Ser Pro Thr Arg Ala
209 30 35 40
210 Tyr Asn Arg Pro Thr Leu Arg Leu Glu Leu Gln Gly Cys Glu
211 45 50 55
212 Val Asn Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys
213 60 65 70
214 Ile Glu Asn Lys Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser
215 75 80
216 Trp Trp Gly Asp Tyr Trp Glu Pro Phe Arg Ala Arg Leu Asn
217 85 90 95
218 Ala Gln Gly Arg Val Asn Ala Trp Gln Ala Lys Ala Asn Asn
219 100 105 110
220 Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu Lys Ile Lys Lys
221 115 120 125
222 Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu Ser Ser
223 130 135 140
224 Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln
225 145 150
226 Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val
227 155 160 165
228 Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val
229 170 175 180
230 Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg
231 185 190 195
232 Val Ile Pro Lys Thr Trp Asn Gln Ser Ile Ala Leu Arg Leu
233 200 205 210
234 Glu Leu Phe Gly Cys Asp Ile Tyr
235 215 218
236
237
238

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

253 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly
254 1 5 10
255 Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
256 15 20 25
257 Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr
258 30 35 40

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/574,735B

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INPUT SET: S36631.raw

Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/482,596

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:39

INPUT SET: S36631.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:39**INPUT SET: S36631.raw**

Line	Original Text	Corrected Text
9	(ii) TITLE OF THE INVENTION: FUSION PROTE	(ii) TITLE OF INVENTION: FUSION PROTEIN W
37	(B) REGISTRATION No.: 30,930	(B) REGISTRATION NUMBER: 30,930
38	(C) REFERENCE/DOCKET No.:CRFC-046	(C) REFERENCE/DOCKET NUMBER:CRFC-046

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:39

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Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/482,596

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:39

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APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:39**INPUT SET: S36631.raw**

Line	Original Text	Corrected Text
9	(ii) TITLE OF THE INVENTION: FUSION PROTE	(ii) TITLE OF INVENTION: FUSION PROTEIN W
37	(B) REGISTRATION No.: 30,930	(B) REGISTRATION NUMBER: 30,930
38	(C) REFERENCE/DOCKET No.:CRFC-046	(C) REFERENCE/DOCKET NUMBER:CRFC-046